AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning on page 7, line 5 as follows:

Fig. 4 shows the amino acid comparison of the UGE homolog belonging to group No. 1 classified by the phylogenetic tree, Ps UGE1 (SEQ ID NO: 2), and Ps UGE2 (SEQ ID NO: 9), with AT1g12780 (SEQ ID NO: 18), At1g63180, (SEQ ID NO: 19), and Ct UGE (SEQ ID NO: 20).

Please amend the paragraph beginning on page 7, line 9 as follows:

Fig. 6 shows the results of detecting the Ps UGE genes in various rice plant varieties via genomic PCR (lane 1: a vector; lane 2: a non-transgenic Nipponbare; lane 3; the Ps UGE transgenic rice; lane 4: Nipponbare; lane 5: IR28; lane 6: Koshihikari; and lane 7: Pokkari). An arrow points to the position of a band corresponding to a 226-bp internal sequence of the Ps UGE gene.

Please amend the paragraph beginning on page 7, line 13 as follows:

Fig. 7 shows the results of detecting the Ps UGE genes in the T0 generation of the Ps UGE transgenic Nipponbare and the F1 generation resulting from the crossing of the T0 generation of Nipponbare and Koshihikari via genomic PCR (upper portion: T0 generation of Nipponbare, lower portion: F1 generation resulting from the crossing of the T0 generation of Nipponbare and Koshihikari). An arrow points to the position of a band corresponding to a 226-bp internal sequence of the Ps UGE gene, V indicates a PCR product obtained when the expression vector Ps UGE1a/pBI221 is used as a template, and NT indicates a genomic PCR product of a non-transgenic rice plant. The upper portion of Fig. 7 shows that bands indicating the presence of the Ps UGE gene were observed in 20 out of the 22 individuals of

the T0 generation of hygromycin tolerant plants. The lower portion (left and right sides) of Fig. 7 shows that of the F1 generation resulting from the crossing of the T0 generation of Nipponbare plants and non-transgenic Koshihikari, the presence of the Ps UGE gene was observed in the genomes of 29 out of the 46 individuals.

Please amend the paragraph beginning on page 7, line 18 as follows:

Fig. 8 shows the confirmation of Ps UGE gene expression in the T0 generation of Nipponbare via RT-PCR. An arrow points to the position of a band corresponding to a 226-bp internal sequence of the Ps UGE gene, V indicates a PCR product obtained when the expression vector Ps UGE1a/pBI221 is used as a template, and NT indicates an RT-PCR product when the first strand cDNA of a non-transgenic rice plant is used as a template. The left portion of Fig. 8 shows bands indicating the transcription of the Ps UGE gene were observed in 20 out of the 22 individuals of the T0 generation of hygromycin tolerant plants, when cDNA was used as a template. In contrast, no band was observed regarding the total RNA used for the synthesis of the first strand cDNA (right portion of Fig. 8).

Please amend the paragraph beginning on page 7, line 24 as follows:

Fig. 10 shows a photograph of rooting of the Ps UGE transgenic rice (35S:Ps UGE1a:nosT; upper right) and that of a plant redifferentiated from the callus of a non-transgenic rice plant (the control; upper left), when they are allowed to grow in a medium containing galactose~~, the~~. The middle section of Fig. 10 shows the number of adventitious roots, while the bottom section of Fig. 10 shows ~~and~~ the maximal length of adventitious roots (cm).

Please amend the paragraph beginning on page 7, line 28 as follows:

Fig. 11 shows a photograph of the shoots of the Ps UGE transgenic rice (35S:Ps UGE1a:nosT; upper right) and that of a plant redifferentiated from the callus of a non-transgenic rice plant (the control; upper left), when they are allowed to grow in a medium containing galactose~~, and~~. The middle section of Fig. 11 shows the maximal length of the shoot (cm) for the control, while the bottom section of Fig. 11 shows the maximal length of the shoot (cm) for 35S:Ps UGE1a:nosT.

Please amend the paragraph beginning on page 8, line 5 as follows:

Fig. 13 shows the results of the test for evaluating the salt stress (NaCl, 3,000 ppm) tolerance of the T0 generation of the Ps UGE transgenic Nipponbare. The degree of leaf blight was visually inspected in the 10th week, and each plant was scored in accordance with the definitions of scores according to the method of IRRI (Table 2). The upper portion of Fig. 13 illustrates the plant at each "score". The lower portion of Fig. 13 shows the observed frequency of each salt tolerance score.

Please amend the paragraph beginning on page 7, line 13 as follows:

Fig. 16 shows the results of genomic PCR on plants selected with galactose (upper portion: the Ps UGE gene; lower portion: the hygromycin tolerant gene). The 6 plants (lanes 1-6 in the upper and lower portions of Fig. 16) in Example 7 were subjected to genomic PCR to confirm the gene introduction using the sense primer (SEQ ID NO: 14) and the antisense primer(SEQ ID NO: 15) of the hygromycin resistant (HPT) gene that is introduced simultaneously with the Ps UGE gene with the internal sequence primers (SEQ ID NOs: 12 and 13) and the expression vector Ps UGE1a/pBI221Hm of the Ps UGE gene that had been

introduced. In the upper portion the presence of the 226-bp band of the Ps UGE gene was assessed and in the lower portion the presence of the 400-bp band of the internal sequence of the hygromycin resistant (HPT) gene was assessed.

Please delete the substitute Sequence Listing filed on August 1, 2006.

Page 52 (Abstract), after the last line, beginning on a new page, please insert the attached Sequence Listing.